chi^2 df P.r(chi^2 >) Pr.exact (Monte-carlo)

X5A 11.99385637 6 6.210600e-02 0.038

X8A 15.00000000 1 1.075112e-04 0.029

X6B 15.00000000 1 1.075112e-04 0.043

X6C 0.01783591 1 8.937575e-01 1.000

X3D 15.23437500 3 1.626928e-03 0.001

X6D 30.00000000 3 1.380057e-06 0.000

X7D 45.00000000 6 4.680213e-08 0.000

X11 15.55782313 15 4.120313e-01 0.223

X10 7.82407407 1 5.155485e-03 0.007

X18 43.33877551 36 1.868235e-01 0.556

X24 18.94304847 6 4.260904e-03 0.033

X107 41.66666667 36 2.378060e-01 0.059

X112 15.05190311 3 1.772827e-03 0.000

X132 19.72796143 21 5.385462e-01 0.266

X144 35.12782369 15 2.358028e-03 0.000

X333 11.48976824 15 7.171663e-01 0.420

X330 29.32291667 21 1.064622e-01 0.217

X294 24.93333333 15 5.084595e-02 0.040

X318 8.04049745 1 4.574297e-03 0.015

X255 57.62500000 45 9.813304e-02 0.008

X222 22.05476190 15 1.063760e-01 0.120

X214 5.51720359 10 8.540656e-01 0.803

X168 8.04049745 1 4.574297e-03 0.009

X150 10.10204082 3 1.771837e-02 0.010

X167 54.15178571 28 2.147364e-03 0.074

LOCUS13 0.07653061 1 7.820553e-01 1.000

I am going to use standard p < .05 as significant.

If I used Bonferroni correction, this would be .05/26 = .00192308. Anything less than this is significant based on Bonferroni correction and means we can reject null hypothesis of HW-equilibrium. However, Bonferroni correction is generally not used here. Presence of potential null alleles affects HW/heterozygosity data because it increases appearance of homozygosity, and also potentially lowers presence of alleles.

LD2 data from genetics package (only did for first pair X5A, X8A), didn’t recognize column names when I entered them manually. This was based on data frame/loci object “y”, which I converted into nancycats format from an excel sheet that had data entered as seen in “Dryad” (refer to KBTO folder). I am considering re-doing work where I enter nancycats format directly. Very frustrated with R – can convert my loci object to genind object with the adegenet package, but can’t provide summary statistics/heterozygosity/make heterozygosity graphs when I follow the summary() command that is recommended.

$Delta

266 267

264 0.05777778 -0.03111111

266 -0.05777778 0.03111111

268 -0.01333333 -0.01333333

270 0.01333333 0.01333333

$T2

T2 df P-val

1.5800719 3.0000000 0.6639168